

P#8

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/294,298

DATE: 08/18/2000
 TIME: 12:46:34

Input Set : A:\48235169.app
 Output Set: N:\CRF3\08182000\I294298.raw

ENTERED

3 <110> APPLICANT: HUGANIR, RICHARD L.
 4 KIM, GJEEHAE
 6 <120> TITLE OF INVENTION: SIGNAL TRANSDUCING SYNAPTIC MOLECULES AND USES THEREOF
 8 <130> FILE REFERENCE: 48235/1699
 10 <140> CURRENT APPLICATION NUMBER: 09/294,298
 11 <141> CURRENT FILING DATE: 1999-04-19
 13 <150> PRIOR APPLICATION NUMBER: 60/082,690
 14 <151> PRIOR FILING DATE: 1998-04-22
 16 <150> PRIOR APPLICATION NUMBER: 60/082,717
 17 <151> PRIOR FILING DATE: 1998-04-23
 19 <160> NUMBER OF SEQ ID NOS: 21
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 4272
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Unknown Organism
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: Description of Unknown Organism: mammalian
 30 SYNGAP-A
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (1..3879, 3883..4272)
 36 <400> SEQUENCE: 1
 37 atg tcc tat gcc ccc ttc aqa gat gta cgg qga ccc cct atg cac cga 48
 38 Met Ser Tyr Ala Pro Phe Arg Asp Val Arg Gly Pro Pro Met His Arg
 39 1 5 10 15
 41 acc caa tac gtt cat tcc ccg tat gac cgt ccc ggt tgg aac ccc cgg 96
 42 Thr Gln Tyr Val His Ser Pro Tyr Asp Arg Pro Gly Trp Asn Pro Arg
 43 20 25 30
 45 ttc tgc atc atc tct qgg aac cag ctg ctc atg ctg gat gag gat gag 144
 46 Phe Cys Ile Ile Ser Gly Asn Gln Leu Met Leu Asp Glu Asp Glu
 47 35 40 45
 49 ata cac ccc ctt ctg atc cgc gac cgg agg agc gag tcc agc cga aac 192
 50 Ile His Pro Leu Leu Ile Arg Asp Arg Ser Glu Ser Ser Arg Asn
 51 50 55 60
 53 aaa ctg ctg aga cgc acc gtc tct gtg cca gtg gag ggg cgg ccc cac 240
 54 Lys Leu Leu Arg Arg Thr Val Ser Val Pro Val Glu Gly Arg Pro His
 55 65 70 75 80
 57 ggc gag cat gaa tac cac ttg ggt cgc tcg agg agg aag agt gtc ccc 288
 58 Gly Glu His Glu Tyr His Leu Gly Arg Ser Arg Arg Lys Ser Val Pro
 59 85 90 95
 61 ggg ggg aaa cag tac agc atg gaa gcc gcc ccc gct gcg ccc ttc cgg 336
 62 Gly Gly Lys Gln Tyr Ser Met Glu Ala Ala Pro Ala Ala Pro Phe Arg
 63 100 105 110
 65 ccc tcg caa ggc ttc ctg agc cgg agg cta aaa agc tcc atc aaa cgt 384
 66 Pro Ser Gln Gly Phe Leu Ser Arg Arg Leu Lys Ser Ser Ile Lys Arg
 67 115 120 125

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69	aca aag tca caa ccc aaa ctt gac cgg acc agc agc ttt cga cag atc	432
70	Thr Lys Ser Gln Pro Lys Leu Asp Arg Thr Ser Ser Phe Arg Gln Ile	
71	130 135 140	
73	ctg cct cgc ttc cga agt gct gac cat gac cgg gcc cgg ctg atg cag	480
74	Leu Pro Arg Phe Arg Ser Ala Asp His Asp Arg Ala Arg Leu Met Gln	
75	145 150 155 160	
77	agc ttc aag gag tct cac tcc cat gag tcc ctg ctg agt ccc agc agt	528
78	Ser Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro Ser Ser	
79	165 170 175	
81	gct gct gag gcc ctg gag ctc aac ctg gat gaa gac tcc att atc aag	576
82	Ala Ala Glu Ala Leu Asn Leu Asp Glu Asp Ser Ile Ile Lys	
83	180 185 190	
85	cca gta cac agc tcc atc ctg ggc cag gag ttc tgc ttt gag gta aca	624
86	Pro Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu Val Thr	
87	195 200 205	
89	aca tcg tct ggg aca aaa tgt ttt gcc tgt cgg tct gca gcc gaa agg	672
90	Thr Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala Glu Arg	
91	210 215 220	
93	gac aaa tgg att gag aat cta cag agg gct gtg aaa ccc aac aag gac	720
94	Asp Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn Lys Asp	
95	225 230 235 240	
97	aac agc cgc cgg gta gat aac gtg ctg aaa cta tgg atc ata gaa gct	768
98	Asn Ser Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile Glu Ala	
99	245 250 255	
101	cga gag ctg ccc aag aag cga tat tac tgc gag tta tgc ctg gag	816
102	Arg Glu Leu Pro Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys Leu Asp	
103	260 265 270	
105	gac atg ctc tat gca cgg acc act tcc aag ccc cgc tca gcc tca gga	864
106	Asp Met Leu Tyr Ala Arg Thr Ser Lys Pro Arg Ser Ala Ser Gly	
107	275 280 285	
109	gac act gtc ttt tgg ggc gag cac ttc gag ttt aac aac ctg cct gct	912
110	Asp Thr Val Phe Trp Gly Glu His Phe Glu Asn Asn Leu Pro Ala	
111	290 295 300	
113	gtc cgg cgc ctg cgg cat ctg tac cgt gac tcg gac aaa aag cgg	960
114	Val Arg Ala Leu Arg Leu His Leu Tyr Arg Asp Ser Asp Lys Lys Arg	
115	305 310 315 320	
117	aag gac aag gca ggc tac gtt ggc ctg gtg act gtt cca gtg gcc	1008
118	Lys Lys Asp Lys Ala Gly Tyr Val Gly Leu Val Thr Val Pro Val Ala	
119	325 330 335	
121	acc ctg gct ggg cgc cac ttc aca gag cag tgg tac ccc gtg acc ctg	1056
122	Thr Leu Ala Gly Arg His Phe Thr Glu Gln Trp Tyr Pro Val Thr Leu	
123	340 345 350	
125	cca aca gga agt ggg ggc tct ggg ggt atg ggc tcg ggg gga gga ggg	1104
126	Pro Thr Gly Ser Gly Gly Ser Gly Gly Met Gly Ser Gly Gly Gly	
127	355 360 365	
129	ggg tca ggg ggc tca ggg ggc aaa ggg aaa gga ggc tgt cct gct	1152
130	Gly Ser Gly Gly Ser Gly Gly Lys Gly Lys Gly Gly Cys Pro Ala	
131	370 375 380	
133	gtg cgg ctg aag gcc cgt tac cag aca atg agt atc ctg ccc atg gag	1200

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134 Val Arg Leu Lys Ala Arg Tyr Gln Thr Met Ser Ile Leu Pro Met Glu	
135 385 390 395 400	
137 cta tat aag gag ttt gca gaa tat gtg acc aac cac tac cgc atg ctg	1248
138 Leu Tyr Lys Glu Phe Ala Glu Tyr Val Thr Asn His Tyr Arg Met Leu	
139 405 410 415	
141 tgt gcc gtg ctg gag ccc gcc ctc aat gtc aag ggc aag gag gag gtc	1296
142 Cys Ala Val Leu Glu Pro Ala Leu Asn Val Lys Gly Lys Glu Val	
143 420 425 430	
145 gct agt gca ctg gtt cac atc ctg caa agc aca ggc aag gcc aag gac	1344
146 Ala Ser Ala Leu Val His Ile Leu Glu Ser Thr Gly Lys Ala Lys Asp	
147 435 440 445	
149 ttc ctt tca gac atg gcc atg tca gag gta gac cgg ttc atg gag cgg	1392
150 Phe Leu Ser Asp Met Ala Met Ser Glu Val Asp Arg Phe Met Glu Arg	
151 450 455 460	
153 gaa cac ctc ata ttc cgc gag aac acg ctc gcc act aaa gcc ata gaa	1440
154 Glu His Leu Ile Phe Arg Glu Asn Thr Leu Ala Thr Lys Ala Ile Glu	
155 465 470 475 480	
157 gag tat atg aga ctg att ggc cag aaa tac ctc aag gat gcc att ggg	1488
158 Glu Tyr Met Arg Leu Ile Gly Gln Lys Tyr Leu Lys Asp Ala Ile Gly	
159 485 490 495	
161 gag ttc atc cgg gct ctg tat gaa tct gag gag aac tgt gaa gta gac	1536
162 Glu Phe Ile Arg Ala Leu Tyr Glu Ser Glu Glu Asn Cys Glu Val Asp	
163 500 505 510	
165 ccc atc aag tgc aca gcg tcc agt ctg gca gag cac cag gcc aac ctg	1584
166 Pro Ile Lys Cys Thr Ala Ser Ser Leu Ala Glu His Gln Ala Asn Leu	
167 515 520 525	
169 cgg atg tgc tgc gag ttg gcc ctg tgc aag gtg gtc aac tcc cat tgc	1632
170 Arg Met Cys Cys Glu Leu Ala Leu Cys Lys Val Val Asn Ser His Cys	
171 530 535 540 540	
173 gtg ttc ccg agg gag ctg aag gag gtg ttt gca tca tgg cgg ctg cgc	1680
174 Val Phe Pro Arg Glu Leu Lys Glu Val Phe Ala Ser Trp Arg Leu Arg	
175 545 550 555 560	
177 tgt gca gag cgg ggc cgg gag gac att gct gac agg ctg atc agc gcc	1728
178 Cys Ala Glu Arg Gly Arg Glu Asp Ile Ala Asp Arg Leu Ile Ser Ala	
179 565 570 575	
181 tcg ctc ttc ctg cgc ttc ctc tgc ccg gcc atc atg tgc ccc agt ctg	1776
182 Ser Leu Phe Leu Arg Phe Leu Cys Pro Ala Ile Met Ser Pro Ser Leu	
183 580 585 590	
185 ttt gga ctg atg cag gag tac cca gat gag cag acc tca cga acc ctc	1824
186 Phe Gly Leu Met Gln Glu Tyr Pro Asp Glu Gln Thr Ser Arg Thr Leu	
187 595 600 605	
189 acc ctc atc gcc aag gtt atc cag aac ctg gcc aac ttt tcc aag ttt	1872
190 Thr Leu Ile Ala Lys Val Ile Gln Asn Leu Ala Asn Phe Ser Lys Phe	
191 610 615 620	
193 acc tca aag gag gac ttc ctg ggc ttc atg aac gag ttt ctg gag ctg	1920
194 Thr Ser Lys Glu Asp Phe Leu Gly Phe Met Asn Glu Phe Leu Glu Leu	
195 625 630 635 640	
197 gag tgg ggt tct atg cag caa ttc ttg tat gag ata tcc aac ctg gac	1968
198 Glu Trp Gly Ser Met Gln Gln Phe Leu Tyr Glu Ile Ser Asn Leu Asp	

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199	645	650	655	
201	aca ctg acc aac agc agc agt ttt gag ggc tac ata gac ttg ggc cgc			2016
202	Thr Leu Thr Asn Ser Ser Ser Phe Glu Gly Tyr Ile Asp Leu Gly Arg			
203	660	665	670	
205	gag ctc tcc aca ctt cac gcc ctg ctc tgg gag gtg ctg ccc cag ctc			2064
206	Glu Leu Ser Thr Leu His Ala Leu Leu Trp Glu Val Leu Pro Gln Leu			
207	675	680	685	
209	agc aag gaa gcc ctc ctg aag ctg ggc cgg ctg ccc cgg ctc ctc agc			2112
210	Ser Lys Glu Ala Leu Leu Lys Leu Gly Pro Leu Pro Arg Leu Leu Ser			
211	690	695	700	
213	gac atc agc aca gcc ctg agg aac cct aac atc caa agg cag ccg agc			2160
214	Asp Ile Ser Thr Ala Leu Arg Asn Pro Asn Ile Gln Arg Gln Pro Ser			
215	705	710	715	720
217	cgc cag agc gag cgc gct cgg tct cag ccc atg gtg ctg cgc ggg ccg			2208
218	Arg Gln Ser Glu Arg Ala Arg Ser Gln Pro Met Val Leu Arg Gly Pro			
219	725	730	735	
221	tca gcc gag atg cag ggc tac atg atg cgg gac ctc aac agc tcc atc			2256
222	Ser Ala Glu Met Gln Gly Tyr Met Met Arg Asp Leu Asn Ser Ser Ile			
223	740	745	750	
225	gac ctt cag tcc ttc atg gct cga ggc ctc aac agc tct atg gac atg			2304
226	Asp Leu Gln Ser Phe Met Ala Arg Gly Leu Asn Ser Ser Met Asp Met			
227	755	760	765	
229	gct cgc ctc ccc tcc cca acc aag gag aaa ccc ccg ccg ccc cct ccc			2352
230	Ala Arg Leu Pro Ser Pro Thr Lys Glu Lys Pro Pro Pro Pro Pro			
231	770	775	780	
233	ggt ggg ggt aaa gac ctg ttc tat gtg agc cgg cca cta ctg gcc cgg			2400
234	Gly Gly Gly Lys Asp Leu Phe Tyr Val Ser Arg Pro Pro Leu Ala Arg			
235	785	790	795	800
237	tcc tcc cca gca tac tgc acg agc agc tcg gac atc aca gag ccg gag			2448
238	Ser Ser Pro Ala Tyr Cys Thr Ser Ser Asp Ile Thr Glu Pro Glu			
239	805	810	815	
241	cag aag atg ctg agt gtc aac aag agt gtg tcc atg ctg gac ctg cag			2496
242	Gln Lys Met Leu Ser Val Asn Lys Ser Val Ser Met Leu Asp Leu Gln			
243	820	825	830	
245	ggc gac ggg cct ggg ggc cgc ctt aac agc agt agt gtt tcc aac ctg			2544
246	Gly Asp Gly Pro Gly Gly Arg Leu Asn Ser Ser Val Ser Asn Leu			
247	835	840	845	
249	gca gct gtt ggg gac ctg ttg cac tca agc cag gct tca ctg aca gca			2592
250	Ala Ala Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu Thr Ala			
251	850	855	860	
253	gcc ttg ggg ttg cgg cct gca cct gcc ggg cgc ctc tcc caa ggg agt			2640
254	Ala Leu Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln Gly Ser			
255	865	870	875	880
257	ggc tct tcc atc aca gca gcc ggc atg cgc ctc agc cag atg ggt gtc			2688
258	Gly Ser Ser Ile Thr Ala Ala Gly Met Arg Leu Ser Gln Met Gly Val			
259	885	890	895	
261	act acg gat ggt gtc ccc gcc cag caa ctg cgc atc cct ctt tcc ttc			2736
262	Thr Thr Asp Gly Val Pro Ala Gln Gln Ile Pro Leu Ser Phe			
263	900	905	910	

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265 cag aac cct ctc ttc cat atg gct gcc gat gga cca ggg ccc cca gca	2784
266 Gln Asn Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro Pro Ala	
267 915 920 925	
269 ggc cat gga ggg agc agt ggc cat ggt cca cct tcc tcc cat cac cac	2832
270 Gly His Gly Ser Ser Gly His Gly Pro Pro Ser Ser His His His	
271 930 935 940	
273 cac cac cac cat cac cga ggg gga gaa ccc cca ggg gac act	2880
274 His His His His His His Arg Gly Gly Glu Pro Pro Gly Asp Thr	
275 945 950 955 960	
277 ttt gcc ccg ttc cat ggc tat agc aag agc gag gac ctc tct aca ggg	2928
278 Phe Ala Pro Phe His Gly Tyr Ser Lys Ser Glu Asp Leu Ser Thr Gly	
279 965 970 975	
281 gtc cct aag ccc cct gcg gcc tcc atc ctt cac agc cac agc tac agt	2976
282 Val Pro Lys Pro Pro Ala Ala Ser Ile Leu His Ser His Ser Tyr Ser	
283 980 985 990	
285 gat gag ttt gga ccc tct ggt act gat ttt acc cgt cgg cag ctc tca	3024
286 Asp Glu Phe Gly Pro Ser Gly Thr Asp Phe Thr Arg Arg Gln Leu Ser	
287 995 1000 1005	
289 ctt cag gac aac cta cag cac atg ctc tcc ccg ccc cag atc acc atc	3072
290 Leu Gln Asp Asn Leu Gln His Met Leu Ser Pro Pro Gln Ile Thr Ile	
291 1010 1015 1020	
293 ggt ccc cag agg cca gct ccc tca ggg cca gga ggg ggc agt ggt ggg	3120
294 Gly Pro Gln Arg Pro Ala Pro Ser Gly Pro Gly Gly Ser Gly Gly	
295 1025 1030 1035 1040	
297 ggc agt ggt ggg ggc ggt ggg ggc cag cca cct ccc ttg cag agg ggc	3168
298 Gly Ser Gly Gly Gly Gly Gly Gln Pro Pro Pro Leu Gln Arg Gly	
299 1045 1050 1055	
301 aaa tct cag cag ttg aca gtg agt gct gcc cag aaa ccc ccg ccg tcc	3216
302 Lys Ser Gln Gln Leu Thr Val Ser Ala Ala Gln Lys Pro Arg Pro Ser	
303 1060 1065 1070	
305 agc ggg aac cta ttg cag tcc ccg gaa cca agt tat ggt cct gcc cgt	3264
306 Ser Gly Asn Leu Leu Gln Ser Pro Glu Pro Ser Tyr Gly Pro Ala Arg	
307 1075 1080 1085	
309 cca ccg caa cag agc ctc agc aaa gag ggc agc att ggg ggc agc ggg	3312
310 Pro Arg Gln Gln Ser Leu Ser Lys Glu Gly Ser Ile Gly Ser Gly	
311 1090 1095 1100	
313 ggc agc ggt ggc gga ggg ggt ggg ggg ctc aag ccc tcc atc acc aag	3360
314 Gly Ser Gly Gly Gly Gly Gly Leu Lys Pro Ser Ile Thr Lys	
315 1105 1110 1115 1120	
317 cag cat tcc cag act cca tcc acg ctg aac ccc acg atg ccg gcc tcg	3408
318 Gln His Ser Gln Thr Pro Ser Thr Leu Asn Pro Thr Met Pro Ala Ser	
319 1125 1130 1135	
321 gag ccg act gta gcc tgg gtg tcc aat atg cct cac ctg tcc gct gac	3456
322 Glu Arg Thr Val Ala Trp Val Ser Asn Met Pro His Leu Ser Ala Asp	
323 1140 1145 1150	
325 atc gag agt gca cac att gag ccg gaa gag tac aag ctg aag gag tac	3504
326 Ile Glu Ser Ala His Ile Glu Arg Glu Glu Tyr Lys Leu Lys Glu Tyr	
327 1155 1160 1165	
329 tcg aag tcc atg gac gag agc cga ctg gac agg gtg aag gag tac gag	3552

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